

## Appendix V

Alignment of instant SEQ ID NO: 1 (nucleotides 1-780) with SEQ ID NO: 1 of Sisk et al.  
 Note: Sisk et al teach a circular plasmid of SEQ ID NO: 1, and the total length of SEQ ID NO: 1 is 6069 nucleotides. Accordingly, nucleotide 6069 is contiguous with nucleotide 1 of Sisk et al.

Score = 1336 bits (723), Expect = 0.0  
 Identities = 723/723 (100%), Gaps = 0/723 (0%)  
 Strand=Plus/Plus

```

Query 58  AGCTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCA 117
          |||||||
Sbjct 1    AGCTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCA 60

Query 118 TAGCCCATATATGGAGTTCGGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACC 177
          |||||||
Sbjct 61  TAGCCCATATATGGAGTTCGGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACC 120

Query 178  GCCCAACGACCCCGCCCATTTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAAT 237
          |||||||
Sbjct 121 GCCCAACGACCCCGCCCATTTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAAT 180

Query 238  AGGGACTTTCCATTGACGTCAATGGGTGGAGTATTACGGTAAACTGCCCACTTGGCAGT 297
          |||||||
Sbjct 181 AGGGACTTTCCATTGACGTCAATGGGTGGAGTATTACGGTAAACTGCCCACTTGGCAGT 240

Query 298  ACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCC 357
          |||||||
Sbjct 241  ACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCC 300

Query 358  CGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCTTACTTGGCAGTACATCTA 417
          |||||||
Sbjct 301  CGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCTTACTTGGCAGTACATCTA 360

Query 418  CGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTGGCAGTACATCAATGGGCGTGG 477
          |||||||
Sbjct 361  CGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTGGCAGTACATCAATGGGCGTGG 420

Query 478  ATAGCGGTTTGACTCACGGGGATTTCCAAAGTCTCCACCCCATTTGACGTCAATGGGAGTTT 537
          |||||||
Sbjct 421  ATAGCGGTTTGACTCACGGGGATTTCCAAAGTCTCCACCCCATTTGACGTCAATGGGAGTTT 480

Query 538  GTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACCTCGCCCCATTGAC 597
          |||||||
Sbjct 481  GTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACCTCGCCCCATTGAC 540

Query 598  GCAAATGGGCGGTAGGCGTGTACGGTGGGAGGCTCTATATAAGCAGAGCTCGTTTAGTGAA 657
          |||||||
Sbjct 541  GCAAATGGGCGGTAGGCGTGTACGGTGGGAGGCTCTATATAAGCAGAGCTCGTTTAGTGAA 600

Query 658  CCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTGGACCTCCATAGAAGACACCGGGA 717
          |||||||
Sbjct 601  CCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTGGACCTCCATAGAAGACACCGGGA 660

Query 718  CCGATCCAGCCTCCGCGGCCGGGAACGGTGCATTGGAACGCGGATTCCCCGTGCCAAGAG 777
          |||||||
Sbjct 661  CCGATCCAGCCTCCGCGGCCGGGAACGGTGCATTGGAACGCGGATTCCCCGTGCCAAGAG 720

Query 778  TGA 780
          |||
Sbjct 721  TGA 723
    
```

Score = 99.0 bits (53), Expect = 7e-24  
 Identities = 53/53 (100%), Gaps = 0/53 (0%)  
 Strand=Plus/Plus

```

Query 5      TGTGAGCGGATAACAATTTCACACAGGAAACAGCTATGACCATGATTACGCCA 57
          |||||||
Sbjct 6017   TGTGAGCGGATAACAATTTCACACAGGAAACAGCTATGACCATGATTACGCCA 6069
    
```